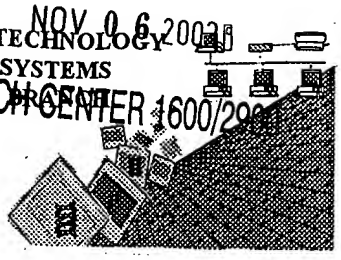

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/647,946
Source: 1600
Date Processed by STIC: 10/29/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**>, **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry directly to (EFFECTIVE 12/01/2003):**
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/2003

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/647,946

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
4	Non-ASCII	The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n/Xaa	"n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

1600

RAW SEQUENCE LISTING DATE: 10/29/2003
PATENT APPLICATION: **US/09/647,946** TIME: 10:00:17

Input Set : **A:\SEQ-APP.txt**
Output Set: **N:\CRF4\10292003\I647946.raw**

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 3 <110> APPLICANT: Brunham, Robert C
 4       University of Manitoba
 6 <120> TITLE OF INVENTION: DNA IMMUNIZATION AGAINST CHLAMYDIA INFECTION
 8 <130> FILE REFERENCE: 1038-1094 MIS:jb
10 <140> CURRENT APPLICATION NUMBER: 09/647,946
11 <141> CURRENT FILING DATE: 2000-12-06
13 <150> PRIOR APPLICATION NUMBER: PCT/CA99/00292
14 <151> PRIOR FILING DATE: 1999-04-07
16 <150> PRIOR APPLICATION NUMBER: 09/055,765
17 <151> PRIOR FILING DATE: 1998-04-07
19 <160> NUMBER OF SEQ ID NOS: 17
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23 <210> SEQ ID NO: 1
24 <211> LENGTH: 393
25 <212> TYPE: PRT
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34 Ala Ser Ser Leu Gln Ala Leu Pro Val Gly Asn Pro Ala Glu Pro Ser
35              20                  25                  30
37 Leu Met Ile Asp Gly Ile Leu Trp Glu Gly Phe Gly Gly Asp Pro Cys
38          35                  40                  45
40 Asp Pro Cys Thr Thr Trp Cys Asp Ala Ile Ser Met Arg Met Gly Tyr
41      50                  55                  60
43 Tyr Gly Asp Phe Val Phe Asp Arg Val Leu Lys Thr Asp Val Asn Lys
44  65                  70                  75                  80
46 Glu Phe Gln Met Gly Asp Lys Pro Thr Ser Thr Thr Gly Asn Ala Thr
47                  85                  90                  95
49 Ala Pro Thr Thr Leu Thr Ala Arg Glu Asn Pro Ala Tyr Gly Arg His
50              100                 105                 110
52 Met Gln Asp Ala Glu Met Phe Thr Asn Ala Ala Cys Met Ala Leu Asn
53          115                 120                 125
55 Ile Trp Asp Arg Phe Asp Val Phe Cys Thr Leu Gly Ala Ser Ser Gly
56      130                 135                 140
58 Tyr Leu Lys Gly Asn Ser Ala Ser Phe Asn Leu Val Gly Leu Phe Gly
59 145                 150                 155                 160
62 Asp Asn Glu Asn Gln Ser Thr Val Lys Thr Asn Ser Val Pro Asn Met
63                 165                 170                 175
65 Ser Leu Asp Gln Ser Val Val Glu Leu Tyr Thr Asp Thr Ala Phe Ser
66              180                 185                 190
68 Trp Ser Val Gly Ala Arg Ala Ala Leu Trp Glu Cys Gly Cys Ala Thr
69          195                 200                 205
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pp 1-5

Does Not Comply
Corrected Diskette Needed

Invalid see item 10 on Error Summary Sheet

RAW SEQUENCE LISTING DATE: 10/29/2003
PATENT APPLICATION: **US/09/647,946** TIME: 10:00:17

Input Set : **A:\SEQ-APP.txt**
Output Set: **N:\CRF4\10292003\I647946.raw**

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72     210                 215                 220
74 Leu Asn Val Leu Cys Asn Ala Ala Glu Phe Thr Ile Asn Lys Pro Lys
75 225                 230                 235                 240
77 Gly Tyr Val Gly Gln Glu Phe Pro Leu Ala Leu Ile Ala Gly Thr Asp
78                 245                 250                 255
80 Ala Ala Thr Gly Thr Lys Asp Ala Ser Ile Asp Tyr Asn Glu Trp Gln
81             260                 265                 270
83 Ala Ser Leu Ala Leu Ser Tyr Arg Leu Asn Met Phe Thr Pro Tyr Ile
84         275                 280                 285
86 Gly Val Lys Trp Ser Arg Ala Ser Phe Asp Ala Asp Thr Ile Arg Ile
87     290                 295                 300
89 Ala Gln Pro Lys Ser Ala Thr Ala Ile Phe Asp Thr Thr Thr Leu Asn
90 305                 310                 315                 320
92 Pro Thr Ile Ala Gly Ala Gly Asp Val Lys Ala Ser Ala Glu Gly Gln
93                 325                 330                 335
95 Leu Gly Asp Thr Met Gln Ile Val Ser Leu Gln Leu Asn Lys Met Lys
96             340                 345                 350
98 Ser Arg Lys Ser Cys Gly Ile Ala Val Gly Thr Thr Ile Val Asp Ala
99         355                 360                 365
101 Asp Lys Tyr Ala Val Thr Val Glu Thr Arg Leu Ile Asp Glu Arg Ala
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122             20                  25                  30
124 Leu Met Ile Asp Gly Ile Leu Trp Glu Gly Phe Gly Gly Asp Pro Cys
125         35                  40                  45
127 Asp Pro Cys Thr Thr Trp Cys Asp Ala Ile Ser Met Arg Met Gly Tyr
128     50                  55                  60
130 Tyr Gly Asp Phe Val Phe Asp Arg Val Leu Lys Thr Asp Val Asn Lys
131 65                  70                  75                  80
133 Glu Phe Gln Met Gly Ala Lys Pro Thr Thr Thr Thr Gly Asn Ala Val
134                 85                  90                  95
136 Ala Pro Ser Thr Leu Thr Ala Arg Glu Asn Pro Ala Tyr Gly Arg His
137             100                 105                 110
139 Met Gln Asp Ala Glu Met Phe Thr Asn Ala Ala Cys Met Ala Leu Asn
140         115                 120                 125
142 Ile Trp Asp Arg Phe Asp Val Phe Cys Thr Leu Gly Ala Ser Ser Gly
143     130                 135                 140
145 Tyr Leu Lys Gly Asn Ser Ala Ser Phe Asn Leu Val Gly Leu Phe Gly
146 145                 150                 155                 160
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RAW SEQUENCE LISTING DATE: 10/29/2003
PATENT APPLICATION: **US/09/647,946** TIME: 10:00:17

Input Set : **A:\SEQ-APP.txt**
Output Set: **N:\CRF4\10292003\I647946.raw**

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149                 165                 170                 175
151 Met Ser Leu Asp Gln Ser Val Val Glu Leu Tyr Thr Asp Thr Ala Phe
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154 Ala Trp Ser Val Gly Ala Arg Ala Ala Leu Trp Glu Cys Gly Cys Ala
155         195                 200                 205
157 Thr Leu Gly Ala Ser Phe Gln Tyr Ala Gln Ser Lys Pro Lys Val Glu
158     210                 215                 220
160 Glu Leu Asn Val Leu Cys Asn Ala Ala Glu Phe Thr Ile Asn Lys Pro
161 225                 230                 235                 240
163 Lys Gly Tyr Val Gly Lys Glu Leu Pro Leu Asp Leu Thr Ala Gly Thr
164                 245                 250                 255
166 Asp Ala Ala Thr Gly Thr Lys Asp Ala Ser Ile Asp Tyr Asn Glu Trp
167             260                 265                 270
169 Gln Ala Ser Leu Ala Leu Ser Tyr Arg Leu Asn Met Phe Thr Pro Tyr
170         275                 280                 285
172 Ile Gly Val Lys Trp Ser Arg Ala Ser Phe Asp Ala Asp Thr Ile Arg
173     290                 295                 300
175 Ile Ala Gln Pro Lys Ser Ala Glu Thr Ile Phe Asp Val Thr Thr Leu
176 305                 310                 315                 320
178 Asn Pro Thr Ile Ala Gly Ala Gly Asp Val Lys Thr Ser Ala Glu Gly
179                 325                 330                 335
181 Gln Leu Gly Asp Thr Met Gln Ile Val Ser Leu Gln Leu Asn Lys Met
182             340                 345                 350
184 Lys Ser Arg Lys Ser Cys Gly Ile Ala Val Gly Thr Thr Ile Val Asp
185         355                 360                 365
187 Ala Asp Lys Tyr Ala Val Thr Val Glu Thr Arg Leu Ile Asp Glu Arg
188     370                 375                 380
190 Ala Ala His Val Asn Ala Gln Phe Arg Phe
191 385                 390
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197 <211> LENGTH: 393
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199 <213> ORGANISM: amino acid
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208              20                  25                  30
210 Leu Met Ile Asp Gly Ile Leu Trp Glu Gly Phe Gly Gly Asp Pro Cys
211          35                  40                  45
213 Asp Pro Cys Thr Thr Trp Cys Asp Ala Ile Ser Met Arg Met Gly Tyr
214      50                  55                  60
216 Tyr Gly Asp Phe Val Phe Asp Arg Val Leu Gln Thr Asp Val Asn Lys
217  65                  70                  75                  80
219 Glu Phe Gln Met Gly Ala Lys Pro Thr Ala Thr Thr Gly Asn Ala Ala
220                 85                  90                  95
222 Ala Pro Ser Thr Cys Thr Ala Arg Glu Asn Pro Ala Tyr Gly Arg His
223             100                 105                 110
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RAW SEQUENCE LISTING DATE: 10/29/2003
PATENT APPLICATION: **US/09/647,946** TIME: 10:00:17

Input Set : **A:\SEQ-APP.txt**
Output Set: **N:\CRF4\10292003\I647946.raw**

```
225 Met Gln Asp Ala Glu Met Phe Thr Asn Ala Ala Tyr Met Ala Leu Asn
226         115                 120                 125
228 Ile Trp Asp Arg Phe Asp Val Phe Cys Thr Leu Gly Ala Thr Ser Gly
229     130                 135                 140
231 Tyr Leu Lys Gly Asn Ser Ala Ser Phe Asn Leu Val Gly Leu Phe Gly
232 145                 150                 155                 160
234 Asp Asn Glu Asn Gln Ser Thr Val Lys Lys Asp Ala Val Pro Asn Met
235                 165                 170                 175
237 Ser Phe Asp Gln Ser Val Val Glu Leu Tyr Thr Asp Thr Thr Phe Ala
238             180                 185                 190
240 Trp Ser Val Gly Ala Arg Ala Ala Leu Trp Glu Cys Gly Cys Ala Thr
241         195                 200                 205
243 Leu Gly Ala Ser Phe Gln Tyr Ala Gln Ser Lys Pro Lys Val Glu Glu
244     210                 215                 220
246 Leu Asn Val Leu Cys Asn Ala Ala Glu Phe Thr Ile Asn Lys Pro Lys
247 225                 230                 235                 240
249 Gly Tyr Val Gly Lys Glu Phe Pro Leu Asp Leu Thr Ala Gly Thr Asp
250                 245                 250                 255
252 Ala Ala Thr Gly Thr Lys Asp Ala Ser Ile Asp Tyr Asn Glu Trp Gln
253             260                 265                 270
255 Ala Ser Leu Ala Leu Ser Tyr Arg Leu Asn Met Phe Thr Pro Tyr Ile
256         275                 280                 285
258 Gly Val Lys Trp Ser Arg Ala Ser Phe Asp Ala Asp Thr Ile Arg Ile
259     290                 295                 300
261 Ala Gln Pro Lys Leu Ala Thr Ala Ile Phe Asp Thr Thr Thr Leu Asn
262 305                 310                 315                 320
264 Pro Thr Ile Ala Gly Ala Gly Glu Val Lys Ala Asn Ala Glu Gly Gln
265                 325                 330                 335
267 Leu Gly Asp Thr Met Gln Ile Val Ser Leu Gln Leu Asn Lys Met Lys
268             340                 345                 350
270 Ser Arg Lys Ser Cys Gly Ile Ala Val Gly Thr Thr Ile Val Asp Ala
271         355                 360                 365
273 Asp Lys Tyr Ala Val Thr Val Glu Thr Arg Leu Ile Asp Glu Arg Ala
274     370                 375                 380
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281 <210> SEQ ID NO: 4
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283 <212> TYPE: PRT
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293             20                  25                  30
295 Leu Met Ile Asp Gly Ile Leu Trp Glu Gly Phe Gly Gly Asp Pro Cys
296         35                  40                  45
298 Asp Pro Cys Thr Thr Trp Cys Asp Ala Ile Ser Met Arg Met Gly Tyr
299     50                  55                  60
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RAW SEQUENCE LISTING DATE: 10/29/2003
PATENT APPLICATION: **US/09/647,946** TIME: 10:00:17

Input Set : **A:\SEQ-APP.txt**
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301 Tyr Gly Asp Phe Val Phe Asp Arg Val Leu Glu Thr Asp Val Asn Lys
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304 Glu Phe His Met Gly Ala Lys Pro Thr Ser Thr Thr Gly Asn Ala Thr
305                  85                  90                  95
307 Ala Pro Thr Thr Leu Thr Ala Arg Glu Asn Pro Ala Tyr Gly Arg His
308             100                 105                 110
310 Met Gln Asp Ala Glu Met Phe Thr Asn Ala Ala Cys Met Ala Leu Asn
311         115                 120                 125
313 Ile Trp Asp Arg Phe Asp Val Phe Cys Thr Leu Gly Ala Thr Ser Gly
314     130                 135                 140
316 Tyr Leu Lys Gly Asn Ser Ala Ser Phe Asn Leu Val Gly Leu Phe Gly
317 145                 150                 155                 160
319 Asp Asn Glu Asn Gln Lys Thr Val Lys Ala Glu Ser Val Pro Asn Met
320                 165                 170                 175
322 Ser Phe Asp Gln Ser Val Val Glu Leu Tyr Thr Asp Thr Thr Phe Ala
323             180                 185                 190
325 Trp Ser Val Gly Ala Arg Ala Ala Leu Trp Glu Cys Gly Cys Ala Thr
326         195                 200                 205
328 Leu Gly Ala Ser Phe Gln Tyr Ala Gln Ser Lys Pro Lys Val Glu Glu
329     210                 215                 220
331 Leu Asn Val Leu Cys Asn Ala Ala Glu Phe Thr Ile Asn Lys Pro Lys
332 225                 230                 235                 240
334 Gly Tyr Val Gly Lys Glu Phe Pro Leu Asp Leu Thr Ala Gly Thr Asp
335                 245                 250                 255
337 Ala Ala Thr Gly Thr Lys Asp Ala Ser Ile Asp Tyr Asn Glu Trp Gln
338             260                 265                 270
340 Ala Ser Leu Ala Leu Ser Tyr Arg Leu Asn Met Phe Thr Pro Tyr Ile
341         275                 280                 285
343 Gly Val Lys Trp Ser Arg Ala Ser Phe Asp Ala Asp Thr Ile Arg Ile
344     290                 295                 300
346 Ala Gln Pro Lys Ser Ala Thr Ala Ile Phe Asp Thr Thr Thr Leu Asn
347 305                 310                 315                 320
349 Pro Thr Ile Ala Gly Ala Gly Asp Val Lys Thr Gly Thr Glu Gly Gln
350                 325                 330                 335
352 Leu Gly Asp Thr Met Gln Ile Val Ser Leu Gln Leu Asn Lys Met Lys
353             340                 345                 350
355 Ser Arg Lys Ser Cys Gly Ile Ala Val Gly Thr Thr Ile Val Asp Ala
356         355                 360                 365
358 Asp Lys Tyr Ala Val Thr Val Glu Thr Arg Leu Ile Asp Glu Arg Ala
359     370                 375                 380
361 Ala His Val Asn Ala Gln Phe Arg Phe
362 385                 390
367 <210> SEQ ID NO: 5
368 <211> LENGTH: 394
369 <212> TYPE: PRT
370 <213> ORGANISM: amino acid
372 <400> SEQUENCE: 5
374 Met Lys Lys Leu Leu Lys Ser Val Leu Val Phe Ala Ala Leu Ser Ser
375   1               5                  10                  15
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The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/29/2003
PATENT APPLICATION: **US/09/647,946** TIME: 10:00:18

Input Set : **A:\SEQ-APP.txt**
Output Set: **N:\CRF4\10292003\I647946.raw**

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The rules require that a line not exceed 72 characters in length. This includes spaces.

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/29/2003
PATENT APPLICATION: **US/09/647,946** TIME: 10:00:18

Input Set : **A:\SEQ-APP.txt**
Output Set: **N:\CRF4\10292003\I647946.raw**

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VERIFICATION SUMMARY DATE: 10/29/2003
PATENT APPLICATION: **US/09/647,946** TIME: 10:00:18

Input Set : **A:\SEQ-APP.txt**
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